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## Full Record

### Details for HUGENEFL:M64347\_AT

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### GeneChip Array Information

Probe Set ID M64347\_at  
 GeneChip Array HumanGeneFL Array  
 Organism Common Name Human

### Probe Design Information

Transcript ID M64347  
 Sequence Type Exemplar sequence  
 Representative Public ID M64347 [NCBI](#)  
 Target Description M64347, class A, 20 probes, 20 in M64347 3336-3720, Human novel growth factor receptor mRNA, 3' cds

### Genomic Alignment of Target Sequence

Assembly April 2003 (NCBI 33)  
 Alignment(s) 

Position	% Identity	Cytoband
chr4: 1771773-1772182 (+) <a href="#">UCSC</a>	93	p16.3

Representative Transcript	UniGene Description	Position
NM_000142 <a href="#">NCBI</a>	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	chr4:1757261-1772237 (+) <a href="#">UCSC</a>
NM_022965 <a href="#">NCBI</a>	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	chr4:1757261-1772237 (+) <a href="#">UCSC</a>

### Public Domain and Genome References

Gene Title fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)  
 Gene Symbol FGFR3 [HGNC](#)  
 Chromosomal Location 4p16.3  
 UniGene ID Hs.1420 [NCBI](#) (FULL LENGTH)  
 Ensembl ENSG00000068078 [Ensembl](#)  
 LocusLink 2261 [NCBI](#)  
 P22607 [EMBL-EBI](#)

SwissProt	Q96T34 <a href="#">EMBL-EBI</a> Q96T35 <a href="#">EMBL-EBI</a> Q96T36 <a href="#">EMBL-EBI</a> Q9NRB6 <a href="#">EMBL-EBI</a>
EC	2.7.1.112
OMIM	134934 <a href="#">NCBI</a>
RefSeq Protein ID	NP_000133 <a href="#">NCBI</a> NP_075254 <a href="#">NCBI</a>
RefSeq	RefSeq Transcript ID RefSeq Title
	NM_000142 <a href="#">NCBI</a> fibroblast growth factor receptor 3 isoform 1 precursor NM_022965 <a href="#">NCBI</a> fibroblast growth factor receptor 3 isoform 2 precursor

## Functional Annotations

	ID	Title	Organism	Type
	<a href="#">DROSGENOME1:143549_AT</a>	breathless	Drosophila	Putative Ortholog
	<a href="#">RAE230A:1369373_AT</a>	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	<a href="#">RAE230B:1384056_AT</a>	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	<a href="#">RAE230B:1384829_AT</a>	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	<a href="#">RG-U34B:RC_AA899336_AT</a>	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	<a href="#">RG-U34C:RC_AI136304_AT</a>	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	<a href="#">RG-U34C:RC_AI145424_AT</a>	fibroblast growth factor receptor 3	Rat	Putative Ortholog
Ortholog	<a href="#">MG-U74AV2:160919_R_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MG-U74AV2:162253_I_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MOE430A:1421841_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MOE430A:1425796_A_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MU11KSUBA:M81342_S_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MOUSE430_2:1421841_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MOUSE430_2:1425796_A_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MOUSE430A_2:1421841_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MOUSE430A_2:1425796_A_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MOUSE430A_2:1425796_A_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog

## GO Biological Process (view graph)

ID	Description	Evidence	Links
165	MAPKKK cascade	experimental evidence	<a href="#">QuickGO</a> <a href="#">AmiGO</a>
1501	skeletal development	predicted/computed	<a href="#">QuickGO</a> <a href="#">AmiGO</a>
7048	oncogenesis	experimental evidence	<a href="#">QuickGO</a> <a href="#">AmiGO</a>
7259	JAK-STAT cascade	experimental	<a href="#">QuickGO</a>

	8543 FGF receptor signaling pathway	evidence experimental evidence	<a href="#">AmiGO</a> <a href="#">QuickGO</a> <a href="#">AmiGO</a>
	GO Cellular Component (view graph)		
	<b>ID</b>	<b>Description</b>	<b>Evidence</b>
Gene Ontology	5887	integral to plasma membrane	experimental evidence
			<a href="#">QuickGO</a> <a href="#">AmiGO</a>
	GO Molecular Function (view graph)		
	<b>ID</b>	<b>Description</b>	<b>Evidence</b>
	5007	fibroblast growth factor receptor activity	experimental evidence
			<a href="#">QuickGO</a> <a href="#">AmiGO</a>
Protein Similarities	<b>Method</b>	<b>ID</b>	<b>Description</b>
	blast	13112048	fibroblast growth factor receptor 3 isoform 2 precursor; hydroxyaryl-protein kinase; tyrosine kinase JTK4 [Homo sapiens]
	blast	13186255	fibroblast growth factor receptor 2 isoform 3 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase [Homo sapiens]
	blast	4503711	fibroblast growth factor receptor 3 isoform 1 precursor; hydroxyaryl-protein kinase; tyrosine kinase JTK4 [Homo sapiens]
	blast	20452380	
Protein Families	<b>Method</b>	<b>ID</b>	<b>Description</b>
	Hanks	<a href="#">FGFR-3</a>	FGR3_HUMAN (FGFR-3) KINASES:5.6.3   PTK Group B membrane spanning protein tyrosine kinases.PTK XV Fibroblast growth factor receptor family .FGFR-3
	ec	<a href="#">ZA70_HUMAN</a>	ZA70_HUMAN EC:2.7.1.112:TYROSINE-PROTEIN KINASE ZAP-70 (EC 2.7.1.112) (70 KDA ZETA-ASSOCIATED PROTEIN) (SYK-RELATED TYROSINE KINASE).
	Hanks	<a href="#">FGFR-3</a>	FGR3_HUMAN (FGFR-3) KINASES:5.6.3   PTK Group B membrane spanning protein tyrosine kinases.PTK XV Fibroblast growth factor receptor family .FGFR-3
	ec	<a href="#">ZA70_HUMAN</a>	ZA70_HUMAN EC:2.7.1.112:TYROSINE-PROTEIN KINASE ZAP-70 (EC 2.7.1.112) (70 KDA ZETA-ASSOCIATED PROTEIN) (SYK-RELATED TYROSINE KINASE).
	<b>Database</b>	<b>ID</b>	<b>Description</b>
	scop	<a href="#">d1gjoa_</a>	d1gjoa_ SCOP:d.144.1.2.  Fibroblast growth factor receptor 2
	scop	<a href="#">d1ev2e1</a>	d1ev2e1 SCOP:b.1.1.4.  Fibroblast growth factor receptor, FGFR
	scop	<a href="#">d1gjoa_</a>	d1gjoa_ SCOP:d.144.1.2.  Fibroblast growth factor receptor 2

Protein Domains	scop	<u>d1ev2e1</u>	d1ev2e1 SCOP:b.1.1.4:] Fibroblast growth factor receptor, FGFR	4.25E-21
	pfam	<u>ig</u>	Immunoglobulin domain	1.6E-5
	pfam	<u>ig</u>	Immunoglobulin domain	3.2E-8
	pfam	<u>pkinase</u>	Protein kinase domain	2.3E-92
	pfam	<u>ig</u>	Immunoglobulin domain	1.6E-5
	pfam	<u>ig</u>	Immunoglobulin domain	3.2E-8
	pfam	<u>pkinase</u>	Protein kinase domain	2.3E-92
	pfam	<u>ig</u>	Immunoglobulin domain	7.3E-8
	InterPro	IPR000719 <u>EMBL-EBI</u>	Protein kinase	
	InterPro	IPR007110 <u>EMBL-EBI</u>	Immunoglobulin-like	
Protein Domains	InterPro	IPR001245 <u>EMBL-EBI</u>	Tyrosine protein kinase	
	InterPro	IPR008266 <u>EMBL-EBI</u>	Tyrosine protein kinase, active site	
	InterPro	IPR003598 <u>EMBL-EBI</u>	Immunoglobulin C-2 type	

## Trans Membrane

ID	Number Of Domains	Probability of Interior N-Terminus
NP_000133	2	0.11005

## Sequence

## Target Sequence

>HUGENEFL:M64347\_AT  
gacttcaaagcaagctgggtattttcatatacaaatcttcttaattgctgtgtgtgtcccaggca  
gggagacgggtttccagggaggggcccggccctgtgtgcagggtccgatgttattagatggt  
acaagtttatataatctatataataatttattgagttttacaagatgtattgttgt  
agacttaacacttcttacgcaatgcttctagagttttatagcctggactgctacctttca  
aagcttggagggaagccgtgaattcagttggttcggttctgtactgttactgggcccctgag  
tctgggcagctgtcccttgcctgcagggccatgggtcagggtggtctcttcttggg  
gcccagtgcatggtggccagaggtgtcacccaaaccggcagggtgcgatt

## Probe Info

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
GACTTCAAAGCAAGCTGGTATTTTC	359	161	3348	Antisense
CATACAAATTCTTCTAATTGCTGTG	360	161	3372	Antisense
AATTCTTCTAATTGCTGTGTGTCCC	361	161	3378	Antisense
TGCTGTGTGTCCCAGGCAGGGAGAC	362	161	3390	Antisense
TGTGTGCAGGTTCCGATGTTATTAG	363	161	3438	Antisense
TCTTACGCAATGCTTCTAGAGTTTT	364	161	3540	Antisense
GCAATGCTTCTAGAGTTTTATAGCC	365	161	3546	Antisense
GAGTTTTATAGCCTGGACTGCTACC	366	161	3558	Antisense
TGCTACCTTTCAAAGCTTGGAGGGA	367	161	3576	Antisense
AAGCTTGGAGGGAAGCCGTGAATTC	368	161	3588	Antisense
TGAATTCAGTTGGTTCGTTCTGTAC	369	161	3606	Antisense
GTTTCGTTCTGTACTGTTACTGGGCC	370	161	3618	Antisense
CTGGGCCCTGAGTCTGGGCAGCTGT	371	161	3636	Antisense
CCTGAGTCTGGGCAGCTGTCCCTTG	372	161	3642	Antisense
TCTGGGCAGCTGTCCCTTGCTTGCC	373	161	3648	Antisense
TCCCTTGCTTGCCTGCAGGGCCATG	374	161	3660	Antisense

GCTTGCCTGCAGGGCCATGGCTCAG	375	161	3666	Antisense
CTTGGGGCCCAGTGCATGGTGGCCA	376	161	3702	Antisense
GTGGCCAGAGGTGTCACCCAAACCG	377	161	3720	Antisense
GTCACCCAAACCGGCAGGTGCGATT	378	161	3732	Antisense

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E.g., search for U46667 in the tool to see the old and current identifiers of the nucleotide sequence in that record.

Note that the original gi number for the nucleotide sequence, 2734632, does not have a corresponding version number. This is true because it was removed from the database (and replaced by 3172140) before the new accession.version system was implemented in Feb. 1999. At that time, each sequence in the GenBank/EMBL/DDBJ database received a version number of 1, even if they had been updated in the past.

In addition, if a GenBank record contains an updated sequence, the Comment field will contain a cross-reference to the gi number of the earlier sequence. (E.g., see U46667 in Entrez.) If you follow the link for that earlier gi number, Entrez will display that version of the GenBank record. Similarly, the Comment field of the older version will have a warning that the sequence has been updated, and will contain a cross-reference to the newer version.

---

More details about sequence identification numbers (GI and accession.version).

Back to sample record.

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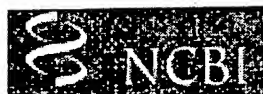
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## Sequence Revision History

Find (Accessions, GI numbers or Fasta style SeqIds) U46667

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### Revision history for U46667

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LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

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GI	Version	Update Date	Status	I	II
3172140	1	<a href="#">Aug 7 1998 9:28 AM</a>	Live	<input checked="" type="radio"/>	<input type="radio"/>
3172140	1	<a href="#">Jun 2 1998 4:31 PM</a>	Dead	<input type="radio"/>	<input checked="" type="radio"/>
2734632	n/a	<a href="#">Jan 3 1998 12:12 AM</a>	Dead	<input type="radio"/>	<input checked="" type="radio"/>
2734632	n/a	<a href="#">Jan 1 1998 12:30 AM</a>	Dead	<input type="radio"/>	<input checked="" type="radio"/>

Accession U46667 was first seen at NCBI on Jan 1 1998 12:30 AM

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Details for HUGENEFL:L17131\_RNA1\_AT  
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## GeneChip Array Information

Probe Set ID L17131\_rnal\_at  
GeneChip Array HumanGeneFL Array  
Organism Common Name Human

## Probe Design Information

Transcript ID L17131\_rnal  
Sequence Type Exemplar sequence  
Representative Public ID L17131 [NCBI](#)  
Target Description L17131, class A, 20 probes, 20 in L17131mRNA#1 1646-2198, Human high mobility group protein (HMG-I(Y)) gene exons 1-8, complete cds

## Sequence

>HUGENEFL:L17131\_RNA1\_AT  
ttgtccaggtgaggcccaagagccctgtggccgccacctgaggtgggctggggctgctcc  
cctaaccctactttcgttccgccactcagccatttccccctcctcagatggggcaccaat  
aacaaggagctcaccctgcccgcctcccaacccccctcctgctcctccctgccccccaagg  
ttctggttccatttttccctcgtgtcacaaactacctctggacagttggtgtgtttttgt  
tcaatgttccattcttccgacatccgtcattgctgctgctaccagcgccaaatgttcatcc  
tcattgcctcctgtttctgcccacgatccccctcccccaagatactcttgtggggaagagg  
ggctggggcatggcaggctgggtgaccgactacccagtcaccaggaaggtggggccctg  
cccctaggatgctgcagcagagtgcagcaagggggcccgaatcgaccataaagggtgtagg  
ggccacctcctccccctgttctgttggggaggggtagccatgatttgtcccagcctgggg  
ctccccctctcgtgttctcatttgcagttacttgaata

Target Sequence

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
TTGTCCAGGTGAGGCCCAAGAGCCC	294	101	1658	Antisense
AGGTGAGGCCCAAGAGCCCTGTGGC	295	101	1664	Antisense
ACCAATAACAAGGAGCTCACCTGTC	296	101	1772	Antisense
TTTTCTCTGTTCAAACTACCTC	297	101	1850	Antisense
CTACCTCTGGACAGTTGTGTTGTTT	298	101	1868	Antisense
TTCCATTCTTCGACATCCGTCATTG	299	101	1904	Antisense
TCTTCGACATCCGTCATTGCTGCTG	300	101	1910	Antisense

Probe Info	GCTACCAGCGCCAAATGTTCATCCT	301	101	1934	Antisense
	TCATCCTCATTGCCTCCTGTTCTGC	302	101	1952	Antisense
	TCATTGCCTCCTGTTCTGCCACGA	303	101	1958	Antisense
	AAGATACTCTTTGTGGGGAAGAGGG	304	101	1994	Antisense
	GCAGGCTGGGTGACCGACTACCCCA	305	101	2030	Antisense
	CCCCTAGGATGCTGCAGCAGAGTGA	306	101	2078	Antisense
	AGCAAGGGGGCCCGAATCGACCATA	307	101	2102	Antisense
	CGAATCGACCATAAAGGGTGTAGGG	308	101	2114	Antisense
	GCCATGATTTGTCCCAGCCTGGGGC	309	101	2174	Antisense
	CTGGGGCTCCCTCTCTGGTTTCCTA	310	101	2192	Antisense
	CTCCCTCTCTGGTTTCCTATTTGCA	311	101	2198	Antisense
	CTCTGGTTTCCTATTTGCAGTTACT	312	101	2204	Antisense
	TTTCCTATTTGCAGTTACTTGAATA	313	101	2210	Antisense

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(L17131)  
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## Full Record

### Details for HUGENEFL:X74801\_AT

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### GeneChip Array Information

**Probe Set ID** X74801\_at  
**GeneChip Array** HumanGeneFL Array  
**Organism Common Name** Human

### Probe Design Information

**Transcript ID** X74801  
**Sequence Type** Exemplar sequence  
**Representative Public ID** X74801 [NCBI](#)  
**Target Description** X74801, class B, 20 probes, 12 in X74801cds 1282-1552: 8 in reverseSequence, 1636-1837, H.sapiens Cctg mRNA for chaperonin

### Genomic Alignment of Target Sequence

**Assembly** April 2003 (NCBI 33)

Alignment(s)	Position	% Identity	Cytoband
chr1: 153495555-153497649 (-) <a href="#">UCSC</a>		100	q22

Overlapping Transcripts	Representative Transcript	UniGene Description	Position
	NM_005998 <a href="#">NCBI</a>	chaperonin containing TCP1, subunit 3 (gamma)	chr1:153495551-153524840 (-) <a href="#">UCSC</a>

### Public Domain and Genome References

**Gene Title** chaperonin containing TCP1, subunit 3 (gamma)  
**Gene Symbol** CCT3 [HGNC](#)  
**Chromosomal Location** 1q23  
**UniGene ID** Hs.1708 [NCBI](#) (FULL LENGTH)  
**Ensembl** ENSG00000163468 [Ensembl](#)  
**LocusLink** 7203 [NCBI](#)  
**SwissProt** AAH06501 [EMBL-EBI](#)  
P49368 [EMBL-EBI](#)  
**OMIM** 600114 [NCBI](#)  
**RefSeq Protein ID** NP\_005989 [NCBI](#)

RefSeq      RefSeq Transcript ID      RefSeq Title  
 NM\_005998 NCBI      chaperonin containing TCP1, subunit 3 (gamma)

### Functional Annotations

	ID	Title	Organism	Type
	<u>ATH1-121501:246830 AT</u>	chaperonin, putative	Arabidopsis	Putative Ortholog
	<u>ATGENOME1:18906 AT</u>	chaperonin, putative	Arabidopsis	Putative Ortholog
	<u>DROSGENOME1:153982 AT</u>		Drosophila	Putative Ortholog
	<u>MG-U74AV2:161238 F AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MG-U74AV2:98153 AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MG-U74CV2:171548 AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOE430A:1416024 X AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOE430A:1426067 X AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOE430A:1448178 A AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOE430A:1449645 S AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOE430A:1451915 AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOE430A:1459987 S AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
Ortholog	<u>MU11KSUBA:C79428 RC F AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MU11KSUBA:L20509 F AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430 2:1416024 X AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430 2:1426067 X AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430 2:1448178 A AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430 2:1449645 S AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430 2:1451915 AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430 2:1459987 S AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430A 2:1416024 X AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430A 2:1426067 X AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430A 2:1448178 A AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430A 2:1449645 S AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430A 2:1451915 AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog

MOUSE430A 2:1459987 S AT chaperonin subunit 3 Mouse (gamma) Curated Ortholog

## GO Biological Process (view graph)

ID	Description	Evidence	Links
6457	protein folding	traceable author statement	<a href="#">QuickGO</a> <a href="#">AmiGO</a>

## GO Cellular Component (view graph)

ID	Description	Evidence	Links
5829	cytosol	not recorded	<a href="#">QuickGO</a> <a href="#">AmiGO</a>
5856	cytoskeleton	traceable author statement	<a href="#">QuickGO</a> <a href="#">AmiGO</a>

Gene Ontology

## GO Molecular Function (view graph)

ID	Description	Evidence	Links
3754	chaperone activity	traceable author statement	<a href="#">QuickGO</a> <a href="#">AmiGO</a>
5524	ATP binding	inferred from electronic annotation	<a href="#">QuickGO</a> <a href="#">AmiGO</a>

Method	ID	Description	E-Value
blast	33873532		0.0
blast	31542292	chaperonin containing TCP1, subunit 3 (gamma); TCP1 (t-complex-1) ring complex, polypeptide 5 [Homo sapiens]	0.0

Protein Similarities

Database	ID	Description	E-Value
scop	<a href="#">d1a6da3</a>	d1a6da3 SCOP:d.56.1.2:  Thermosome	4.08E-25
scop	<a href="#">d1gmla</a>	d1gmla_ SCOP:c.8.5.2:  Thermosome	1.01E-57
scop	<a href="#">d1a6da1</a>	d1a6da1 SCOP:a.129.1.2:  Thermosome	4.81E-83
pfam	<a href="#">cpn60_TCP1</a>	TCP-1/cpn60 chaperonin family	5.7E-210
InterPro	<a href="#">IPR002423</a> <a href="#">EMBL-EBI</a>	Chaperonin Cpn60/TCP-1	
InterPro	<a href="#">IPR001844</a> <a href="#">EMBL-EBI</a>	Chaperonin Cpn60	
InterPro	<a href="#">IPR002194</a> <a href="#">EMBL-EBI</a>	Chaperonin TCP-1	
InterPro	<a href="#">IPR008950</a> <a href="#">EMBL-EBI</a>	GroEL-like chaperone, ATPase	

Protein Domains

## Sequence

>HUGENEFL:X74801\_AT  
 atgactggtgtggaacaatggccatacagggtgtgtgccaggccctagaggtcattcct  
 cgtaccctgatccagaactgtggggccagcaccatccgtctacttacctcccttcggggcc  
 aagcacacccaggagaactgtgagacctgggggtgtaaattggtgagacgggtactttggtg  
 gacatgaaggaactgggcataatgggagccattggctgtgaagctgcagacttataagaca  
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 aaaggcgatgaccagagccggcaaggcggggtcctgatgctggccaggagtgagtgtta  
 ggcaaggctacttcaatgcacagaaccagcagagtctcccccttttcctgagccagagtgc  
 caggaacactgtggacgtctttgttcagaagggatcaggttggggggcagcccccaggtcc  
 ctttctgtccagctcagttttccaaaagacactgacatgtaattcttctctattgtaag  
 gtttccatttagtttgcttccgatgattaaatctaagtca

Target Sequence

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
-----------------------	---------	---------	------------------------------	--------------

Probe Info	ATGACTGGTGTGGAACAATGGCCAT	60	345	1294	Antisense
	GAACAATGGCCATACAGGGCTGTTG	61	345	1306	Antisense
	CTGATCCAGAACTGTGGGGCCAGCA	62	345	1360	Antisense
	CAGAACTGTGGGGCCAGCACCATCC	63	345	1366	Antisense
	TGTGGGGCCAGCACCATCCGTCTAC	64	345	1372	Antisense
	CTGGGCATATGGGAGCCATTGGCTG	65	345	1486	Antisense
	ATATGGGAGCCATTGGCTGTGAAGC	66	345	1492	Antisense
	GAGCCATTGGCTGTGAAGCTGCAGA	67	345	1498	Antisense
	TTGGCTGTGAAGCTGCAGACTTATA	68	345	1504	Antisense
	GAGACGGCAGTTCTGCTACTGCGAA	69	345	1540	Antisense
	GCAGTTCTGCTACTGCGAATTGATG	70	345	1546	Antisense
	ATTGATGACATCGTTTCAGGCCACA	71	345	1564	Antisense
	GTGCTAGGCAAGGCTACTTCAATGC	72	345	1648	Antisense
	GGCAAGGCTACTTCAATGCACAGAA	73	345	1654	Antisense
	GCTACTTCAATGCACAGAACCAGCA	74	345	1660	Antisense
	CACAGAACCAGCAGAGTCTCCCCTT	75	345	1672	Antisense
	GAGCCAGAGTGCCAGGAACACTGTG	76	345	1702	Antisense
	CACTGACATGTAATTCTTCTCTATT	77	345	1804	Antisense
	TAGTTTGCTTCCGATGATTAAATCT	78	345	1843	Antisense
	GCTTCCGATGATTAAATCTAAGTCA	79	345	1849	Antisense

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-> (1) All Descriptions  
(HG3523)  
-> all probe sets  
(7129)  
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(X74801)  
-> (1) All Descriptions  
(L17131)  
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Queries**Full Record****Details for HUGENEFL:U15008\_AT**  
**Full Screen****NetAffx Links** [Cluster Members](#)  
[Consensus/Exemplar](#)**GeneChip Array Information****Probe Set ID** U15008\_at  
**GeneChip  
Array** HumanGeneFL Array  
**Organism  
Common  
Name** Human**Probe Design Information****Transcript ID** U15008  
**Sequence  
Type** Exemplar sequence  
**Representative  
Public ID** U15008 [NCBI](#)  
**Target** U15008, class A, 20 probes, 20 in U15008 25-433, Human SnRNP core protein  
**Description** Sm D2 mRNA, complete cds**Genomic Alignment of Target Sequence****Assembly** April 2003 (NCBI 33)  

	Position	% Identity	Cytoband
<b>Alignment(s)</b>	chr19: 50882580-50883664 (-) <a href="#">UCSC</a>	98	q13.32

	Representative Transcript	UniGene Description	Position
<b>Overlapping Transcripts</b>	NM_004597 <a href="#">NCBI</a>	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	chr19:50882558- 50887282 (-) <a href="#">UCSC</a>
	NM_177542 <a href="#">NCBI</a>	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	chr19:50882558- 50887282 (-) <a href="#">UCSC</a>

**Public Domain and Genome References****Gene Title** small nuclear ribonucleoprotein D2 polypeptide 16.5kDa  
**Gene Symbol** SNRPD2 [HGNC](#)  
**Chromosomal  
Location** 19q13.2  
**UniGene ID** Hs.424327 [NCBI](#) (FULL LENGTH)  
**Ensembl** ENSG00000125743 [Ensembl](#)  
**LocusLink** 6633 [NCBI](#)  
**SwissProt** P43330 [EMBL-EBI](#)  
**OMIM** 601061 [NCBI](#)

RefSeq Protein ID NP\_004588 [NCBI](#)  
NP\_808210 [NCBI](#)

RefSeq Transcript ID RefSeq Title  
NM\_004597 [NCBI](#) small nuclear ribonucleoprotein polypeptide D2  
NM\_177542 [NCBI](#) small nuclear ribonucleoprotein polypeptide D2

### Functional Annotations

	ID	Title	Organism	Type
Ortholog	<a href="#">ATH1-121501:266482_AT</a>	small nuclear ribonucleo protein D2 -related	Arabidopsis	Putative Ortholog
	<a href="#">C.ELEGANS:172931_X_AT</a>	small nuclear ribonucleoprotein D2 like	Celegans	Putative Ortholog
	<a href="#">DROSGENOME1:153483_AT</a>		Drosophila	Putative Ortholog
	<a href="#">MG-U74AV2:95049_AT</a>	small nuclear ribonucleoprotein D2	Mouse	Curated Ortholog
	<a href="#">MOE430A:1452680_AT</a>	small nuclear ribonucleoprotein D2	Mouse	Curated Ortholog
	<a href="#">MU11KSUBA:AA271024_S_AT</a>	small nuclear ribonucleoprotein D2	Mouse	Curated Ortholog
	<a href="#">MOUSE430_2:1452680_AT</a>	small nuclear ribonucleoprotein D2	Mouse	Curated Ortholog
	<a href="#">MOUSE430A_2:1452680_AT</a>	small nuclear ribonucleoprotein D2	Mouse	Curated Ortholog

### GO Biological Process (view graph)

ID	Description	Evidence	Links
245	spliceosome assembly	traceable author statement	<a href="#">QuickGO</a> <a href="#">AmiGO</a>
6371	mRNA splicing	traceable author statement	<a href="#">QuickGO</a> <a href="#">AmiGO</a>

### GO Cellular Component (view graph)

ID	Description	Evidence	Links
5681	spliceosome complex	traceable author statement	<a href="#">QuickGO</a> <a href="#">AmiGO</a>
5732	small nucleolar ribonucleoprotein complex	inferred from electronic annotation	<a href="#">QuickGO</a> <a href="#">AmiGO</a>
30532	small nuclear ribonucleoprotein complex	traceable author statement	<a href="#">QuickGO</a> <a href="#">AmiGO</a>

### GO Molecular Function (view graph)

ID	Description	Evidence	Links
8248	pre-mRNA splicing factor activity	inferred from electronic annotation	<a href="#">QuickGO</a> <a href="#">AmiGO</a>

	Method	ID	Description	E-Value
Protein Similarities	blast	4759158	small nuclear ribonucleoprotein polypeptide D2; snRNP core protein D2. [Homo sapiens]	1.0E-62
	blast	26337731		3.0E-62
	blast	4759158	small nuclear ribonucleoprotein polypeptide D2; snRNP core protein D2 [Homo sapiens]	1.0E-62
	blast	26337731		3.0E-62

Database	ID	Description	E-Value
scop	<a href="#">d1b34b</a>	d1b34b_SCOP:b.38.1.1: D2 core SNRNP	1.85E-



Protein Domains	scop	<a href="#">d1b34b</a>	protein	28
			d1b34b_SCOP:b.38.1.1; D2 core SNRNP	1.85E-28
	pfam	<a href="#">LSM</a>	LSM domain	1.1E-16
	pfam	<a href="#">LSM</a>	LSM domain	1.1E-16
	InterPro	<a href="#">IPR001163</a>	Small nuclear ribonucleoprotein (Sm protein)	
		<a href="#">EMBL-EBI</a>		

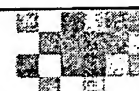
## Sequence

>HUGENEFL:U15008\_AT  
 accatcatgagcctcctcaacaagcccaagagtgagatgacccagaggagctgcagaag  
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 aatacccaagtgtcatcaactgccgcaacaataagaaactcctggcgcggtgaaggcc  
 ttcgataggcactgcaacatggtgctggagaacgtgaaggagatgtggactgaggtacc  
 aagagtggcaagggaagaagaagtccaagccagtcaacaaagaccgctacatctccaag  
 atgttcctgcgcggggactcagtcacgtggtcctgcggaaccgctcatcgccggcaag  
 tagggcgccgtgctgttgacagaactcactcctctgtcctatgaagaccgctgccatt  
 ggtgttgagaata

Probe Info	Probe Sequence(5'-3')	Probe		Probe Interrogation Position	Strandedness
		X	Y		
	ACCATCATGAGCCTCCTCAACAAGC	99	211	37	Antisense
	AGTGAGATGACCCCAGAGGAGCTGC	100	211	67	Antisense
	AACACCGGTCCACTCTCTGTGCTCA	101	211	115	Antisense
	GGTCCACTCTCTGTGCTCACACAGT	102	211	121	Antisense
	CTCTCTGTGCTCACACAGTCAGTCA	103	211	127	Antisense
	GTGCTCACACAGTCAGTCAAGAACA	104	211	133	Antisense
	TCAGTCAAGAACAATACCCAAGTGC	105	211	145	Antisense
	AATACCCAAGTGCTCATCAACTGCC	106	211	157	Antisense
	CAAGTGCTCATCAACTGCCGCAACA	107	211	163	Antisense
	CGCGTGAAGGCCTTCGATAGGCACT	108	211	205	Antisense
	AAGGCCTTCGATAGGCACTGCAACA	109	211	211	Antisense
	TTCGATAGGCACTGCAACATGGTGC	110	211	217	Antisense
	GTACCCAAGAGTGGCAAGGGCAAGA	111	211	271	Antisense
	TACATCTCCAAGATGTTCTGCGCG	112	211	325	Antisense
	TCAGTCATCGTGGTCTGCGGAACC	113	211	355	Antisense
	TAGGGGCCGCCTGTCTGTTGACAGA	114	211	397	Antisense
	TGACAGAACTCACTCCTCTGTCCTA	115	211	415	Antisense
	CTCCTCTGTCCTATGAAGACCGCTG	116	211	427	Antisense
	TGTCCTATGAAGACCGCTGCCATTG	117	211	433	Antisense
	ACCGCTGCCATTGGTGTGAGAATA	118	211	445	Antisense



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→ (2) All Descriptions  
(AFFX-BioDn-5)  
→ (2) All Descriptions  
(AFFX-BioB-M)  
→ (1) All Descriptions  
(M12625\_at)

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## Full Record

### Details for HUGENEFL:AFFX-BIOB-M\_ST

#### Full Screen

NetAffx Links [Cluster Members](#)  
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### GeneChip Array Information

Probe Set ID: AFFX-BioB-M\_st  
GeneChip Array: HumanGeneFL Array  
Organism Common Name: Human

### Probe Design Information

Transcript ID: AFFX-BioB-M  
Sequence Type: Control sequence  
Representative Public ID: J04423 [NCBI](#)  
Target Description: J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)

### Sequence

>HUGENEFL:AFFX-BIOB-M\_ST  
gccggagttttacggcaatatcatcaccacacgcacttatcaggaacgcctcgatacgct  
ggaaaaagtgcgcgatgccgggatcaaagtcgttctggcggcattgtgggcttaggcga  
aacggtaaaagatcgccgggattattgctgcaactggcaaacctgccgacgccgcgga  
aagcgtgccaatcaacatgctggtgaagggtgaaaggcacgcgcgcttgccgataacgatga  
tgtcgatgcctttgattt

#### Target Sequence

#### Probe Info

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
GATGATATTGCCGTA AAACTCCGGC	201	11	483	Sense
TGTGGTGATGATATTGCCGTA AAAC	202	11	489	Sense
TAAGTGCGTGTGGTGATGATATTGC	203	11	497	Sense
GTTCTGTATAAGTGCGTGTGGTGAT	204	11	505	Sense
ATCGAGGCGTTTCTGTATAAGTGCGT	205	11	513	Sense
GCATCGCGCACTTTTCCAGCGTAT	206	11	536	Sense
GATCCCGGCATCGCGCACTTTTCC	207	11	543	Sense
GACTTTGATCCCGGCATCGCGCACT	208	11	549	Sense
CGCCAGAACAGACTTTGATCCCGGC	209	11	559	Sense
CCCACAATGCCGCCAGAACAGACTT	210	11	569	Sense

TGCAGCAATAATCCGGCGCGATCTT	211	11	611	Sense
TTGCCAGTTGCAGCAATAATCCGGC	212	11	619	Sense
CGGCAGGTTTGCCAGTTGCAGCAAT	213	11	627	Sense
ATGTTGATTGGCACGCTTCCGGCG	214	11	656	Sense
CACCAGCATGTTGATTGGCACGCTT	215	11	663	Sense
TTCACCTTCACCAGCATGTTGATTG	216	11	671	Sense
AGCGGCGTGCCTTTCACCTTCACCA	217	11	683	Sense
CATCATCGTTATCGGCAAGCGGCGT	218	11	700	Sense
GCATCGACATCATCGTTATCGGCAA	219	11	707	Sense
AAATCAAAGGCATCGACATCATCGT	220	11	716	Sense

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5\_st)  
-> (1) All Descriptions  
(AFFX-BioB-M\_st)  
-> (1) All Descriptions  
(HG613)  
-> (2) All Descriptions  
(AFFX-BioDn-5)  
-> (2) All Descriptions  
(AFFX-BioB-M)

-> Genotyping  
Queries

## Full Record

### Details for HUGENEFL:AFFX-BIODN-5\_ST

#### Full Screen

NetAffx Links [Cluster Members](#)  
[Consensus/Exemplar](#)

### GeneChip Array Information

Probe Set ID AFFX-BioDn-5\_st  
GeneChip Array HumanGeneFL Array  
Organism Common Name Human

### Probe Design Information

Transcript ID AFFX-BioDn-5  
Sequence Type Control sequence  
Representative Public ID J04423 [NCBI](#)  
Target Description J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)

### Sequence

#### Target Sequence

>HUGENEFL:AFFX-BIODN-5\_ST  
gggaaaactgtcgccagttgtgcacttttacaaagccgcaaaggcagcaggctaccggacg  
gcaggttataaacgggtcgccctctggcagcgaaaagaccccggaaggtttacgcaatagc  
gacgcgctggcgttacagcgcaacagcagcctgcagctggattacgcaacagtaaatcct  
tacaccttcgcagaaccacttcgcgcacatcatcagcgcgaagagggcagaccgata  
gaatcattggtaatgagcgccggtattacgcgcgcttg

#### Probe Info

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
GTGCACAACTGGCGACAGTTTCCC	281	11	49	Sense
GGCTTGTAAGTGCACAACTGGCG	282	11	60	Sense
GCTGCCTTTGCGGCTTGTAAGT	283	11	71	Sense
GGTAGCCTGCTGCCTTTGCGGCTG	284	11	79	Sense
CCGTCGCGTAGCCTGCTGCCTTTGC	285	11	85	Sense
CAGCGCGTCGCTATTGCGTAAACCT	286	11	153	Sense
GTAACGCCAGCGCGTCGCTATTGCG	287	11	160	Sense
TTGCGCTGTAACGCCAGCGCGTCGC	288	11	167	Sense
TGCTGTTGCGCTGTAACGCCAGCGC	289	11	172	Sense
TGCAGGCTGCTGTTGCGCTGTAACG	290	11	179	Sense

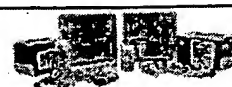
TCCAGCTGCAGGCTGCTGTTGCGCT	291	11	185	Sense
TGCGTAATCCAGCTGCAGGCTGCTG	292	11	192	Sense
TTACTGTTGCGTAATCCAGCTGCAG	293	11	199	Sense
CGGTCTGCCCTCTTGCGCGCTGATG	294	11	261	Sense
GATTCTATCGGTCTGCCCTCTTGCG	295	11	269	Sense
TACCAATGATTCTATCGGTCTGCCC	296	11	276	Sense
CTCATTACCAATGATTCTATCGGTC	297	11	281	Sense
TCCGGCGCTCATTACCAATGATTCT	298	11	288	Sense
CGCGTAATCCGGCGCTCATTACCAA	299	11	295	Sense
CAAGCGCGCGTAATCCGGCGCTCAT	300	11	301	Sense

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→ (1) All Descriptions  
(HG4011-  
HT4804\_s\_at)  
→ (1) All Descriptions  
(AFFX-BioDn-  
5\_st)  
→ (1) All Descriptions  
(AFFX-BioB-M\_st)  
→ (1) All Descriptions  
(HG613)  
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## Full Record

### Details for HUGENEFL:X15880\_AT

#### Full Screen

NetAffx Links [Cluster Members](#)  
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### GeneChip Array Information

Probe Set ID X15880\_at  
GeneChip Array HumanGeneFL Array  
Organism Common Name Human

### Probe Design Information

Transcript ID X15880  
Sequence Type Exemplar sequence  
Representative Public ID X15880 [NCBI](#)  
Target X15880, class C, 20 probes; 20 in all\_X15880 1690-2273, Human mRNA for  
Description collagen VI alpha-1 C-terminal globular domain

### Genomic Alignment of Target Sequence

Assembly April 2003 (NCBI 33)  
Alignment(s) Position % Identity Cytoband  
chr21: 46280561-46281145 (+) [UCSC](#) 100 q22.3  
Overlapping Representative UniGene Description Position  
Transcripts Transcript  
NM\_001848 collagen, type VI, alpha chr21:46257869-46281164 (+)  
[NCBI](#) 1 [UCSC](#)

### Public Domain and Genome References

Gene Title collagen, type VI, alpha 1  
Gene Symbol COL6A1 [HGNC](#)  
Chromosomal Location 21q22.3  
UniGene ID Hs.415997 [NCBI](#) (FULL LENGTH)  
Ensembl ENSG00000142156 [Ensembl](#)  
LocusLink 1291 [NCBI](#)  
P12109 [EMBL-EBI](#)  
Q7Z645 [EMBL-EBI](#)  
Q8TBN2 [EMBL-EBI](#)  
Q9BSA8 [EMBL-EBI](#)  
OMIM 120220 [NCBI](#)

RefSeq Protein ID NP\_001839 NCBI

RefSeq Transcript ID RefSeq Title  
NM\_001848 NCBI collagen, type VI, alpha 1 precursor

### Functional Annotations

	ID	Title	Organism	Type
Ortholog	<a href="#">MG-U74AV2:162459_F_AT</a>	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
	<a href="#">MG-U74AV2:95493_AT</a>	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
	<a href="#">MOE430A:1448590_AT</a>	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
	<a href="#">MU11KSUBB:X66405_S_AT</a>	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
	<a href="#">MOUSE430_2:1448590_AT</a>	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
	<a href="#">MOUSE430A_2:1448590_AT</a>	procollagen, type VI, alpha 1	Mouse	Curated Ortholog

### GO Biological Process (view graph)

ID	Description	Evidence	Links
7155	cell adhesion	non-traceable author statement	<a href="#">QuickGO</a> <a href="#">AmiGO</a>

### GO Cellular Component (view graph)

ID	Description	Evidence	Links
5578	extracellular matrix	inferred from electronic annotation	<a href="#">QuickGO</a> <a href="#">AmiGO</a>
5589	collagen type VI	non-traceable author statement	<a href="#">QuickGO</a> <a href="#">AmiGO</a>

### Gene Ontology

### GO Molecular Function (view graph)

ID	Description	Evidence	Links
5194	cell adhesion molecule activity	inferred from electronic annotation	<a href="#">QuickGO</a> <a href="#">AmiGO</a>
5201	extracellular matrix structural constituent	inferred from electronic annotation	<a href="#">QuickGO</a> <a href="#">AmiGO</a>

### Protein Similarities

Method	ID	Description	E-Value
blast	15011913		0.0
blast	13878903		0.0

### Protein Domains

Database	ID	Description	E-Value
scop	<a href="#">d1atza_</a>	d1atza_SCOP:c.62.1.1:  von Willebrand factor A3 domain	3.63E-37
pfam	<a href="#">vwa</a>	von Willebrand factor type A domain	9.6E-24
pfam	<a href="#">vwa</a>	von Willebrand factor type A domain	4.7E-32
pfam	<a href="#">vwa</a>	von Willebrand factor type A domain	2.7E-35
pfam	<a href="#">Collagen</a>	Collagen triple helix repeat (20 copies)	2.4E-11
pfam	<a href="#">Collagen</a>	Collagen triple helix repeat (20 copies)	3.8E-14
pfam	<a href="#">Collagen</a>	Collagen triple helix repeat (20 copies)	3.3E-10
pfam	<a href="#">Collagen</a>	Collagen triple helix repeat (20 copies)	2.6E-11
InterPro	<a href="#">IPR008161</a> <a href="#">EMBL-EBI</a>	Collagen helix repeat	
InterPro	<a href="#">IPR002035</a> <a href="#">EMBL-EBI</a>	von Willebrand factor, type A	

InterPro IPR008160 Collagen triple helix repeat  
EMBL-EBI

### Sequence

>HUGENEFL:X15880\_AT

agcaagacgcctctcggggcctgtgccgcactagcctccctctcctctgtcccatagct  
 ggtttttcccaccaatcctcacctaacagttactttacaattaaactcaaagcaagctct  
 tctcctcagcttggggcagccattggcctctgtctcgttttgggaaaccaaggtcaggag  
 gccgttgacagacataaatctcggcgactcggccccgtctcctgagggctcctgctggtgac  
 cggcctggaccttggccctacagccctggaggccgctgctgaccagcactgaccccgacc  
 tcagagagtactcgcaggggctggtgctgactcaagaccctcgagattaacggtgctaa  
 ccccgctgctcctccctcccgcagagactggggcctggactggacatgagagcccttg  
 gtgccacagagggtgtgtcttactagaaacaacgcaaacctctccttctcagaatagt  
 gatgtgttcgacgttttatcaaaggccccctttctatgttcatgttagtttgcctctc  
 tgtgtttttttctgaaccatatccatgttgctgacttttccaa

Target  
Sequence

Probe Info	Probe Sequence(5'-3')	Probe		Probe Interrogation Position	Strandedness
		X	Y		
	AGCAAGACGCCTCTCGGGGCCTGTG	76	317	1702	Antisense
	AAACTCAAAGCAAGCTCTTCTCCTC	77	317	1804	Antisense
	AAAGCAAGCTCTTCTCCTCAGCTTG	78	317	1810	Antisense
	TCTCCTCAGCTTGGGGCAGCCATTG	79	317	1822	Antisense
	GCCATTGGCCTCTGTCTCGTTTTGG	80	317	1840	Antisense
	GCAGACATAAATCTCGGCGACTCGG	81	317	1888	Antisense
	GCCCCGTCTCCTGAGGGTCTGCTG	82	317	1912	Antisense
	TGGCCCTACAGCCCTGGAGGCCGCT	83	317	1954	Antisense
	TCAGAGAGTACTCGCAGGGGCGCTG	84	317	2002	Antisense
	AGTACTCGCAGGGGCGCTGGCTGCA	85	317	2008	Antisense
	GGCGCTGGCTGCACTCAAGACCCTC	86	317	2020	Antisense
	GGACATGAGAGCCCCCTTGGTGCCAC	87	317	2104	Antisense
	GAGAGCCCCCTTGGTGCCACAGAGGG	88	317	2110	Antisense
	CCCTTGGTGCCACAGAGGGCTGTGT	89	317	2116	Antisense
	GTGCCACAGAGGGCTGTGTCTTACT	90	317	2122	Antisense
	CAGAGGGCTGTGTCTTACTAGAAAC	91	317	2128	Antisense
	CTCCTTCCTCAGAATAGTGATGTGT	92	317	2164	Antisense
	TTTTTCTGAACCATATCCATGTTGC	93	317	2248	Antisense
	TGAACCATATCCATGTTGCTGACTT	94	317	2254	Antisense
	ATATCCATGTTGCTGACTTTTCCAA	95	317	2260	Antisense





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- > (1) All Descriptions (HG3523)
- > all probe sets (7129)

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**Details for HUGENEFL:U23752\_AT**

**Full Screen**

NetAffx Links [Cluster Members](#)  
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**GeneChip Array Information**

Probe Set ID U23752\_at  
GeneChip Array HumanGeneFL Array  
Organism Common Name Human

**Probe Design Information**

Transcript ID U23752  
Sequence Type Exemplar sequence  
Representative Public ID U23752 [NCBI](#)  
Target U23752, class A, 20 probes, 20 in U23752 1679-1919, Human SOX-11 mRNA,  
Description complete cds

**Genomic Alignment of Target Sequence**

Assembly April 2003 (NCBI 33)  
Alignment(s) Position % Identity Cytoband  
chr2: 5856192-5856457 (+) [UCSC](#) 99 p25.2

Overlapping Transcripts	Representative Transcript	UniGene Description	Position
	NM_003108 <a href="#">NCBI</a>	SRY (sex determining region Y)-box 11	chr2:5854537-5863255 (+) <a href="#">UCSC</a>

**Public Domain and Genome References**

Gene Title SRY (sex determining region Y)-box 11  
Gene Symbol SOX11 [HGNC](#)  
Chromosomal Location 2p25  
UniGene ID Hs.432638 [NCBI](#) (FULL LENGTH)  
Ensembl ENSG00000176887 [Ensembl](#)  
LocusLink 6664 [NCBI](#)  
SwissProt P35716 [EMBL-EBI](#)  
OMIM 600898 [NCBI](#)  
RefSeq Protein ID NP\_003099 [NCBI](#)

RefSeq  
RefSeq Transcript ID RefSeq Title  
NM\_003108 [NCBI](#) SRY-box 11

## Functional Annotations

	ID	Title	Organism	Type
Ortholog	<a href="#">RAE230A:1387275_AT</a>	SRY-box containing gene 11	Rat	Putative Ortholog
	<a href="#">RG-U34A:AJ004858_AT</a>	SRY-box containing gene 11	Rat	Putative Ortholog

## GO Biological Process (view graph)

ID	Description	Evidence	Links
6355	regulation of transcription, DNA-dependent	inferred from electronic annotation	<a href="#">QuickGO</a> <a href="#">AmiGO</a>
7399	neurogenesis	traceable author statement	<a href="#">QuickGO</a> <a href="#">AmiGO</a>

Gene Ontology  
GO Cellular Component (view graph)

ID	Description	Evidence	Links
5634	nucleus	inferred from electronic annotation	<a href="#">QuickGO</a> <a href="#">AmiGO</a>

## GO Molecular Function (view graph)

ID	Description	Evidence	Links
3677	DNA binding	inferred from electronic annotation	<a href="#">QuickGO</a> <a href="#">AmiGO</a>

Method	ID	Description	E-Value
blast	4507161	SRY-box 11; SRY (sex-determining region Y)-box 11; SRY-related HMG-box gene 11; transcription factor SOX-11 [Homo sapiens]	0.0
blast	23831472		0.0

## Protein Similarities

Database	ID	Description	E-Value
scop	<a href="#">d1i11a</a>	d1i11a_SCOP:a.21.1.1:  Sox-5	2.36E-19
pfam	<a href="#">HMG_box</a>	HMG (high mobility group) box	1.1E-33
InterPro	<a href="#">IPR000910</a>	HMG1/2 (high mobility group) box	
	<a href="#">EMBL-EBI</a>		

## Protein Domains

## Sequence

## Target Sequence

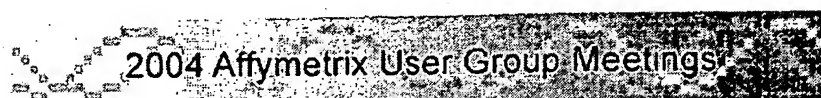
>HUGENEFL:U23752\_AT  
 cttcctttatcgtgtctcaaggtagttgcatacctagtctggagttgtgattatntttccc  
 aaaaaatgtgtttttgtaattactattttcttttctgaaattcgtgattgcaacaaagg  
 cagagggggcggcgcggcggaggggaggtaggaccgctccggaaggcgtgtttgaagc  
 ttgtcgtctttgaagtctggaagacgtctgcagaggaccttttggcagcacaaactgtt  
 actctaggagttggtggagatatt

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
CTTCCTTTATCGTGTCTCAAGGTAG	503	219	1691	Antisense
TTATCGTGTCTCAAGGTAGTTGCAT	504	219	1697	Antisense
TCGTGTCTCAAGGTAGTTGCATACC	505	219	1700	Antisense
AAGGTAGTTGCATACCTAGTCTGGA	506	219	1709	Antisense
GTAGTTGCATACCTAGTCTGGAGTT	507	219	1712	Antisense

Probe Info	GTTGCATACCTAGTCTGGAGTTGTG	508	219	1715	Antisense
	TACCTAGTCTGGAGTTGTGATTATT	509	219	1721	Antisense
	CTAGTCTGGAGTTGTGATTATTTTC	510	219	1724	Antisense
	TGTGATTATTTTCCCAAAAATGTG	511	219	1736	Antisense
	TTTTCTGAAATTCGTGATTGCAAC	512	219	1781	Antisense
	GCTCCGGAAGGCGCTGTTTGAAGCT	513	219	1847	Antisense
	GCTGTTTGAAGCTTGTCGGTCTTTG	514	219	1859	Antisense
	TGAAGCTTGTCGGTCTTTGAAGTCT	515	219	1865	Antisense
	TTGTCGGTCTTTGAAGTCTGGAAGA	516	219	1871	Antisense
	TGGAAGACGTCTGCAGAGGACCCTT	517	219	1889	Antisense
	AAGACGTCTGCAGAGGACCCTTTTG	518	219	1892	Antisense
	GCAGAGGACCCTTTTGGCAGCACAA	519	219	1901	Antisense
	AGCACAACTGTTACTCTAGGGAGTT	520	219	1919	Antisense
	ACTGTTACTCTAGGGAGTTGGTGGA	521	219	1925	Antisense
	ACTCTAGGGAGTTGGTGGAGATATT	522	219	1931	Antisense

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     -> (1) All Descriptions  
         (U23752\_at)  
     -> (1) All Descriptions  
         (HG1800-  
         HT1823\_at)  
     -> (1) All Descriptions  
         (U15008\_at)  
     -> (1) All Descriptions  
         (HG3523)  
 -> Genotyping  
     **Queries**

**Full Record****Details for HUGENEFL:M12625\_AT****Full Screen**

NetAffx Links [Cluster Members](#)  
[Consensus/Exemplar](#)

**GeneChip Array Information**

Probe Set ID M12625\_at  
 GeneChip Array HumanGeneFL Array  
 Organism Common Name Human

**Probe Design Information**

Transcript ID M12625  
 Sequence Type Exemplar sequence  
 Representative Public ID M12625 [NCBI](#)  
 Target Description M12625, class B, 20 probes, 13 in M12625mRNA 893-1259: 7 in reverseSequence, 1599-1683, Human lecithin-cholesterol acyltransferase mRNA, complete cds, with 5' and 3' flanking DNA sequences

**Genomic Alignment of Target Sequence**

Assembly April 2003 (NCBI 33)  
 Alignment(s) Position % Identity Cytoband  
 chr16: 67749925-67750484 (-) [UCSC](#) 100 q22.1

Overlapping Transcripts	Representative Transcript	UniGene Description	Position
M12625 <a href="#">NCBI</a>	lecithin-cholesterol acyltransferase	chr16:67749888-67754507 (-) <a href="#">UCSC</a>	

**Public Domain and Genome References**

Gene Title lecithin-cholesterol acyltransferase  
 Gene Symbol [LCAT](#) [HGNC](#)  
 Chromosomal Location 16q22.1  
 UniGene ID Hs.387239 [NCBI](#) (FULL LENGTH)  
 Ensembl ENSG00000103080 [Ensembl](#)  
 LocusLink 3931 [NCBI](#)  
 SwissProt AAP88750 [EMBL-EBI](#)  
 P04180 [EMBL-EBI](#)  
 EC 2.3.1.43  
 OMIM 606967 [NCBI](#)

RefSeq Protein ID NP\_000220 NCBI

RefSeq RefSeq Transcript ID RefSeq Title  
NM\_000229 NCBI lecithin-cholesterol acyltransferase precursor

## Functional Annotations

	ID	Title	Organism	Type
Ortholog	<a href="#">MG-U74AV2:103023 AT</a>	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
	<a href="#">MG-U74AV2:161759 R AT</a>	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
	<a href="#">MOE430A:1417043 AT</a>	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
	<a href="#">MU11KSUBA:J05154 S AT</a>	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
	<a href="#">RAE230A:1367887 AT</a>	lecithin cholesterol acyltransferase	Rat	Curated Ortholog
	<a href="#">RG-U34A:X54096 AT</a>	lecithin cholesterol acyltransferase	Rat	Curated Ortholog
	<a href="#">MOUSE430 2:1417043 AT</a>	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
	<a href="#">MOUSE430A 2:1417043 AT</a>	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog

## GO Biological Process (view graph)

ID	Description	Evidence	Links
6629	lipid metabolism	inferred from electronic annotation	<a href="#">QuickGO</a> <a href="#">AmiGO</a>

## GO Cellular Component (view graph)

ID	Description	Evidence	Links
5576	extracellular	not recorded	<a href="#">QuickGO</a> <a href="#">AmiGO</a>

## Gene Ontology

## GO Molecular Function (view graph)

ID	Description	Evidence	Links
4607	phosphatidylcholine-sterol O-acyltransferase activity	inferred from electronic annotation	<a href="#">QuickGO</a> <a href="#">AmiGO</a>
8415	acyltransferase activity	inferred from electronic annotation	<a href="#">QuickGO</a> <a href="#">AmiGO</a>
16740	transferase activity	inferred from electronic annotation	<a href="#">QuickGO</a> <a href="#">AmiGO</a>

	Method	ID	Description	E-Value
Protein Similarities	blast	32879837		0.0
	blast	4557892	lecithin-cholesterol acyltransferase precursor [Homo sapiens]	0.0

	Method	ID	Description	E-Value
Protein Families	ec	<a href="#">LCAT_HUMAN</a>	LCAT_HUMAN	1.85E-171
			EC:2.3.1.43:PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE).	

Database	ID	Description	E-Value
----------	----	-------------	---------

scop d1tca d1tca\_\_ SCOP:c.69.1.17:| Triacylglycerol lipase 5.3E-8  
 pfam LACT Lecithin:cholesterol acyltransferase 1.7E-182

InterPro IPR003386 Lecithin:cholesterol acyltransferase  
EMBL-EBI

**Protein  
Domains**

InterPro IPR008262 Lipase, active site  
EMBL-EBI

**Trans Membrane**

ID	Number Of Domains	Probability of Interior N-Terminus
NP_000220	2	0.05945

**Sequence**

>HUGENEFL:M12625\_AT  
 cttcaactacacaggccgtgacttccaacgcttctttgcagacctgcactttgaggaagg  
 ctggtacatgtggctgcagtcacgtgacctcctggcaggactcccagcacctgggtgga  
 agtatactgtctttacggcgtgggctgcccacgccccgcacctacatctacgaccacgg  
 cttccctacacggacctgtgggtgtgctctatgaggatggatgacacgggtggcgac  
 ccgcagcaccgagctctgtggcctgtggcaggccgcagccacagcctgtgcacctgt  
 gccctgcacgggatacagcatctcaacatgggtcttcagcaacctgacctggagcacat  
 caatgccatcctgtgggtgcctaccgccagggtccccctgcatccccgactgccagccc  
 agagccccgcctcctgaataaagaccttctttgtctaccgtaagccctgatggctatgt  
 ttcaggttgaaggaggcactagagtcacactaggtttcactcctcaccagccacagg  
 ctgagtgctgtgtgcagtg

**Target  
Sequence**

Probe Info	Probe Sequence(5'-3')	Probe		Probe Interrogation Position	Strandedness
		X	Y		
	CTTCAACTACACAGGCCGTGACTTC	152	127	1161	Antisense
	CTACACAGGCCGTGACTTCCAACGC	153	127	1167	Antisense
	CCAACGCTTCTTTGCAGACCTGCAC	154	127	1185	Antisense
	CCTGCACTTTGAGGAAGGCTGGTAC	155	127	1203	Antisense
	CATGTGGCTGCAGTCACGTGACCTC	156	127	1227	Antisense
	GCTGCAGTCACGTGACCTCCTGGCA	157	127	1233	Antisense
	CCTGGCAGGACTCCAGCACCTGGT	158	127	1251	Antisense
	GGACCCTGTGGGTGTGCTCTATGAG	159	127	1353	Antisense
	TGTGCTCTATGAGGATGGTGATGAC	160	127	1365	Antisense
	GGCGACCCGCAGCACCGAGCTCTGT	161	127	1395	Antisense
	CCTGACCCTGGAGCACATCAATGCC	162	127	1503	Antisense
	GCACATCAATGCCATCCTGCTGGGT	163	127	1515	Antisense
	CATCCTGCTGGGTGCCTACCGCCAG	164	127	1527	Antisense
	CTTTGCTACCGTAAGCCCTGATGGC	165	127	1611	Antisense
	TACCGTAAGCCCTGATGGCTATGTT	166	127	1617	Antisense
	AAGCCCTGATGGCTATGTTTCAGGT	167	127	1623	Antisense
	CTATGTTTCAGGTTGAAGGGAGGCA	168	127	1635	Antisense
	GGAGGCACTAGAGTCCCACACTAGG	169	127	1653	Antisense
	GTCCCACACTAGGTTTCACTCCTCA	170	127	1665	Antisense
	CACAGGCTCAGTGCTGTGTGCAGTG	171	127	1695	Antisense

